

CLAIMS

1. In a system including a database of values of properties of polymers of chemical units, a method for determining the composition of a sample polymer of chemical units having a known molecular length, comprising steps of:
 - 5 (A) selecting, from the database, candidate polymers of chemical units having the same length as the sample polymer of chemical units and for which the value of a predetermined property is similar to the value of the predetermined property of the sample polymer of chemical units;
 - (B) performing an experiment on the sample polymer of chemical units;
 - 10 (C) measuring properties of the sample polymer of chemical units resulting from the experiment; and
 - (D) eliminating, from the candidate polymers of chemical units, polymers of chemical units having properties that do not correspond to the experimental results.
- 15 2. The method of claim 1, further comprising a step of:
 - (E) repeatedly performing the step (D) until the number of candidate polymers of chemical units falls below a predetermined threshold.
3. The method of claim 1, wherein the predetermined property is molecular weight.
4. A method for identifying a population of polymers of chemical units having the same
20 property as a sample polymer of chemical units, comprising:
 - determining a property of a sample polymer of chemical units;
 - comparing the property of the sample polymer to a reference database of polymers of known sequence and known properties to identify a population of polymers of chemical units having the same property as a sample polymer of chemical units, wherein the reference
25 database of polymers includes identifiers corresponding to the chemical units of the polymers, each of the identifiers including a field storing a value corresponding to the property.
5. The method of claim 4, wherein the step of determining a property of the sample polymer involves the use of mass spectrometry to determine the molecular weight of the polymer.

6. The method of claim 4, wherein the mass spectrometry is MALDI which detects molecular weight with an accuracy of approximately one Dalton.
7. The method of claim 4, wherein polymer is reduced to at least two fragments and the property of the polymer is the size of the fragments and wherein the step of detection involves strong ion exchange chromatography.
8. The method of claim 6, wherein the MALDI analysis is performed on a MALDI surface having a protein coated thereon.
9. The method of claim 6, wherein the sample polymer is isolated from a cell surface.
10. A method for identifying a subpopulation of polymers having a property in common with a sample polymer of chemical units, comprising:
 - (A) applying an experimental constraint to the polymer to modify the polymer,
 - (B) detecting a property of the modified polymer;
 - (C) identifying a population of polymers of chemical units having the same molecular length as the sample polymer; and
 - 15 (D) identifying a subpopulation of the identified population of polymers having the same property as the modified polymer by eliminating, from the identified population of polymers, polymers having properties that do not correspond to the modified polymer.
11. The method of claim 10, further comprising repeating steps (A), (B), and (D) on the modified polymer to identify a second subpopulation within the subpopulation of polymers having a second property in common with the twice modified polymer.
12. The method of claim 11, further comprising repeatedly performing the steps (A), (B), and (D) on the modified polymer until the number of polymers within the subpopulation falls below a predetermined threshold.
13. The method of claim 12, wherein the predetermined threshold of polymers within the subpopulation is two polymers and wherein the method is performed to identify the sequence of the polymer.
14. The method of claim 12, wherein the experimental constraints applied to the polymer are different for each repetition.

15. The method of claim 10, wherein the experimental constraint applied to the polymer is digestion with an exoenzyme.
16. The method of claim 10, wherein the experimental constraint applied to the polymer is digestion with an endoenzyme.
- 5 17. The method of claim 10, wherein the experimental constraint applied to the polymer is selected from the group consisting of restriction endonuclease digestion; chemical digestion; chemical modification; interaction with a binding compound; chemical peeling; and enzymatic modification.
18. The method of claim 10, wherein the property of the polymer is molecular weight.
- 10 19. The method of claim 10, wherein the population of polymers of chemical units includes every polymer sequence having the molecular weight of the sample polymer.
20. The method of claim 10, wherein the population of polymers of chemical units includes less than every polymer sequence having the molecular weight of the sample polymer.
- 15 21. The method of claim 10, wherein the step of detection involves the use of mass spectrometry to determine the molecular weight of the polymer.
22. The method of claim 21, wherein the mass spectrometry is matrix assisted laser desorption ionization which detects molecular weight with an accuracy of approximately one
20 Dalton.
23. The method of claim 10, wherein polymer is reduced to at least two fragments and the property of the polymer is the size of the fragments and wherein the step of detection involves strong ion exchange chromatography.
24. The method of claim 10, wherein the step of identifying includes selecting the
25 population of polymers of chemical units from a database including molecular weights of polymers of chemical units.

25. The method of claim 24, wherein the database includes identifiers corresponding to chemical units of a plurality of polymers, each of the identifiers including a field storing a value corresponding to a property of the corresponding chemical unit.
26. A method for compositional analysis of chemical units of a sample polymer,
5 comprising:
 (A) applying an experimental constraint to the sample polymer to modify the sample polymer,
 (B) detecting a property of the modified sample polymer;
 (C) comparing the modified sample polymer to a reference database of polymers of
10 identical size as the polymer, wherein the polymers of the reference database have also been subjected to the same experimental constraint as the sample polymer, wherein the comparison provides a compositional analysis of the sample polymer.
27. The method of claim 26, wherein the step of detection involves capillary
15 electrophoresis.
28. The method of claim 26, wherein the experimental constraint applied to the polymer involves complete degradation of the polymer into individual chemical units, and wherein the compositional analysis reveals the number and type of units within the polymer.
29. The method of claim 26, wherein the step of detection involves matrix assisted laser
20 desorption ionization mass spectrometry.
30. The method of claim 29, wherein the experimental constraint applied to the polymer involves incomplete enzymatic digestion of the polymer and wherein steps (A), (B), and (C) are repeated until the number of polymers within the reference database falls below a predetermined threshold, and wherein the compositional analysis reveals the identity of a
25 sequence of chemical units of the polymer.
31. The method of claim 24, wherein the reference database includes identifiers corresponding to chemical units of a plurality of polymers, each of the identifiers including a field storing a value corresponding to a property of the corresponding chemical unit.
32. A method for sequencing a polymer, comprising:

- (A) applying an experimental constraint to the polymer to modify the polymer,
(B) detecting a property of the modified polymer;
(C) identifying a population of polymers having the same molecular length as the
5 of the sample polymer and having molecular weights similar to the molecular weight
of the sample polymer;
(D) identifying a subpopulation of the identified population of polymers having the
same property as the modified polymer by eliminating, from the identified
population of polymers, polymers having properties that do not correspond to
the modified polymer;
10 (E) repeating steps (A), (B), and (D) by applying additional experimental
constraints to the polymer and identifying additional subpopulations of
polymers until the number of polymers within the subpopulation is one and the
sequence of the polymer may be identified.
33. A method for identifying a polysaccharide-protein interaction, comprising:
15 contacting a protein-coated MALDI surface with a polysaccharide containing sample
to produce a polysaccharide-protein-coated MALDI surface,
removing unbound polysaccharide from the polysaccharide-protein-coated MALDI
surface, and
performing MALDI mass spectrometry to identify the polysaccharide that specifically
20 interacts with the protein coated on the MALDI surface.
34. The method of claim 33, wherein a MALDI matrix is added to the polysaccharide-
protein-coated MALDI surface.
35. The method of claim 33, further comprising applying an experimental constraint to the
polysaccharide bound on the polysaccharide-protein-coated MALDI surface before
25 performing the MALDI mass spectrometry analysis.
36. The method of claim 35, wherein the experimental constraint applied to the polymer is
digestion with an exoenzyme.

37. The method of claim 35, wherein the experimental constraint applied to the polymer is digestion with an endoenzyme.
38. The method of claim 35, wherein the experimental constraint applied to the polymer is selected from the group consisting of restriction endonuclease digestion; chemical digestion;
5 chemical modification; and enzymatic modification.